

From: Page, Thurman  
Sent: Thursday, April 07, 2005 5:38 PM  
To: Basi, Nirmal; STIC-Biotech/ChemLib  
Cc: Page, Thurman  
Subject: RE: Rush search for 09/719,485

Importance: High

RUSH SEARCH APPROVED

Thurman K. Page  
SPE, Art Unit 1615  
Technology Center 1600  
571-272-0602

-----Original Message-----

From: Basi, Nirmal  
Sent: Thursday, April 07, 2005 5:36 PM  
To: Page, Thurman  
Subject: FW: Rush search for 09/719,485

Need approval for a rush search, Cristina is out until Monday.

I am seeking approval for a RUSH sequence search, as indicated below. If approved, could you please forward the search to STIC and cc a copy to me.

Examiner: Nirmal S. Basi  
Art Unit 1646  
Office: Remsen Building, Room 4D68  
Mail Room: Remsen Building, room 4C70

Sequence search:

App. #: 09/719,485  
Result format: Paper.

Title: **CLONING AND IDENTIFICATION OF THE MOTLIN RECEPTOR**

Inventors: Feighner et al

Priority Date: 6/12/98

Please search:

- i) SEQ ID NOS: 1-5
- ii) ~~Nucleic acid encoding the polypeptide of SEQ ID NO: 1~~

Search issued, commercial and interference databases.

Thanks,  
Nirmal S. Basi

\*\*\*\*\*

STAFF USE ONLY

Searcher: Arnold  
Searcher Phone: 2-2532  
Date Searcher Picked up: 4/12/05  
Date Completed: 4/12/05  
Searcher Prep/Rev. Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search

NA#: \_\_\_\_\_ AA#: \_\_\_\_\_  
Interference: \_\_\_\_\_ SPDI: \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure#: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIS: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other(Specify): \_\_\_\_\_



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 1981 ACTGAG 3246

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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE  
 1. Sheppard, P.O., Jaspers, S.R., Deisher, T.A. and Bishop, P.D.  
 Method of forming a peptide-receptor complex with zslg33 and  
 therapeutic use thereof  
 Patent: WO 0138355-A 11 31-MAY-2001;  
 JOURNAL (US)  
 Zymogenetics, Inc./Qualifiers  
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| 35 | 453.5 | 21.0 | 295 | 2 | Q7PDF2     | Q7pdf2 anopheles g |
| 36 | 453   | 21.0 | 556 | 1 | CAPR_DROME | Q8itc7 drosophila  |
| 37 | 437   | 20.3 | 418 | 2 | O17239     | O17239 caenorhabdi |
| 38 | 436   | 20.2 | 346 | 2 | Q6VYH4     | Q6vyh4 heliothis z |
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## ALIGNMENTS

## RESULT 1

## MTLR HUMAN

ID MTLR HUMAN STANDARD; PRT; 412 AA.

AC O43193;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Motilin receptor (G protein-coupled receptor 38).

GN Name=MLNR; Synonyms=GPR38, MTLR, MTLR1;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM A).

RX MEDLINE=98110578; PubMed=9441746; DOI=10.1006/geno.1997.5069;

RA McKee K.K., Tan C.P., Palyha O.C., Liu J., Feighner S.D.,

RA Hreniuk D.L., Smith R.G., Howard A.D., van der Ploeg L.H.T.;

RT "Cloning and characterization of two human G protein-coupled receptor

RT genes (GPR38 and GPR39) related to the growth hormone secretagogue and

RT neurotensin receptors.";

RL Genomics 46:426-434(1997).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORMS A AND B).

RX MEDLINE=99316084; PubMed=10381885; DOI=10.1126/science.284.5423.2184;

RA Feighner S.D., Tan C.P., McKee K.K., Palyha O.C., Hreniuk D.L.,

RA Pong S.-S., Austin C.P., Figueroa D., MacNeil D., Cascieri M.A.,

RA Nargund R., Bakshi R., Abramovitz M., Stocco R., Kargman S.,

RA O'Neill G., van Der Ploeg L.H.T., Evans J., Patchett A.A., Smith R.G.,

RA Howard A.D.;

RT "Receptor for motilin identified in the human gastrointestinal

RT system.";

RL Science 284:2184-2188(1999).

RN [3]

RP SEQUENCE FROM N.A.

RX PubMed=15057823; DOI=10.1038/nature02379;

RA Dunham A., Matthews L.H., Burton J., Ashurst J.L., Howe K.L.,

RA Ashcroft K.J., Beare D.M., Burford D.C., Hunt S.E.,

RA Griffiths-Jones S., Jones M.C., Keenan S.J., Oliver K., Scott C.E.,

RA Ainscough R., Almeida J.P., Ambrose K.D., Andrews D.T.,

RA Ashwell R.I.S., Babbage A.K., Baggeley C.L., Bailey J., Bannerjee R.,

RA Barlow K.F., Bates K., Beasley H., Bird C.P., Bray-Allen S.,

RA Brown A.J., Brown J.Y., Burrill W., Carder C., Carter N.P.,

RA Chapman J.C., Clamp M.E., Clark S.Y., Clarke G., Clee C.M.,

RA Clegg S.C., Cobley V., Collins J.E., Corby N., Coville G.J.,

RA Deloukas P., Dhami P., Dunham I., Dunn M., Earthrowl M.E.,

RA Ellington A.G., Faulkner L., Frankish A.G., Frankland J., French L.,

RA Garner P., Garnett J., Gilbert J.G.R., Gilson C.J., Ghorri J.,

RA Grafham D.V., Gribble S.M., Griffiths C., Hall R.E., Hammond S.,

RA Harley J.L., Hart E.A., Heath P.D., Howden P.J., Huckle E.J.,

RA Hunt P.J., Hunt A.R., Johnson C., Johnson D., Kay M., Kimberley A.M.,

RA King A., Laird G.K., Langford C.J., Lawlor S., Leongamornlert D.A.,

RA Lloyd D.M., Lloyd C., Loveland J.E., Lovell J., Martin S.,

RA Mashreghi-Mohammadi M., McLaren S.J., McMurray A., Milne S.,

RA Moore M.J.F., Nickerson T., Palmer S.A., Pearce A.V., Peck A.I.,  
RA Pelan S., Phillimore B., Porter K.M., Rice C.M., Searle S.,  
RA Sehra H.K., Showkeen R., Skuce C.D., Smith A., Stewart C.A.,  
RA Sycamore N., Tester J., Thomas D.W., Tracey A., Tromans A., Tubby B.,  
RA Wall M., Wallis J.M., West A.P., Whitehead S.L., Willey D.L.,  
RA Wilming L., Wray P.W., Wright M.P., Young L., Coulson A., Durbin R.,  
RA Hubbard T., Sulston J.E., Beck S., Bentley D.R., Rogers J., Ross M.T.,  
RA "The DNA sequence and analysis of human chromosome 13.",  
RA Nature 428:522-528 (2004).  
RN [4]  
RP FUNCTION.  
RX MEDLINE=21219832; PubMed=1132507; DOI=10.1385/ENDO.14.1.009;  
RA Smith R.G., Leonard R., Bailey A.R.T., Palyha O.C., Feighner S.D.,  
RA Tan C.P., McKee K.K., Pong S.-S., Griffin P.R., Howard A.D.,  
RA "Growth hormone secretagogue receptor family members and ligands.",  
RT Endocrine 14:9-14 (2001).  
CC -!- FUNCTION: Receptor for motilin.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event-Alternative splicing; Named isoforms=2;  
CC Name=A;  
CC IsoId=O43193-1; Sequence=Displayed;  
CC Name=B;  
CC IsoId=O43193-2; Sequence=VSP\_001894;  
CC -!- TISSUE SPECIFICITY: Expressed only in thyroid, stomach, and bone marrow.  
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; AF034632; AAC26081.1; -;  
CC EMBL; AL137000; CAC19107.1; -;  
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CC GO; GO:0004930; F:G-protein coupled receptor activity; TAS.  
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CC GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . ; TAS.  
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CC PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
CC PROSITE; PS00262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW Alternative splicing; G-protein coupled receptor; Glycoprotein; Transmembrane.  
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FT DOMAIN 1 35 1 (Potential).  
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FT DOMAIN 57 74 2 (Potential).  
FT TRANSMEM 75 94 Extracellular (Potential).  
FT DOMAIN 95 112 3 (Potential).  
FT TRANSMEM 113 134 Cytoplasmic (Potential).  
FT DOMAIN 135 157 4 (Potential).  
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DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Orphan G protein-coupled receptor.  
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RP MEDLINE=20092336; PubMed=10628755; DOI=10.1210/me.14.1.160;  
RA Palyha O.C., Feighner S.D., Tan C.P., McKee K.K., Hreniuk D.L.,  
RA Gao Y.D., Schleim K.D., Yang L., Morriello G.J., Nargund R.,  
RA Patchett A.A., Howard A.D., Smith R.G.;  
RT "Ligand activation domain of human orphan growth hormone (GH) secretagogue receptor (GHS-R) conserved from Pufferfish to humans.";  
Mol. Endocrinol. 14:160-169 (2000).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
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## ORIGIN

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 QY 121 GTGACGCGCTGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180  
 DB 121 GTGACGCGCTGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180  
 QY 181 ATGCTGATCGGCGCTGACCGGACATCGGACCACTGTAAGTGGGAGGATG 240  
 DB 181 ATGCTGATCGGCGCTGACCGGACATCGGACCACTGTAAGTGGGAGGATG 240  
 QY 241 GCGGTGCGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300  
 DB 241 GCGGTGCGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300  
 QY 301 TCGGCGCGCGGGGCTGCGGCGCGCTGCTGCGCGCGCTGCTGCTGCTGCTGCTG 360  
 DB 301 TCGGCGCGCGGGGCTGCGGCGCGCTGCTGCGCGCGCTGCTGCTGCTGCTGCTG 360  
 QY 361 TGGCACTAGCGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420  
 DB 361 TGGCACTAGCGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420  
 QY 421 TGGCGCGCGCTGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480  
 DB 421 TGGCGCGCGCTGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480  
 QY 481 GTGCTGCGGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540  
 DB 481 GTGCTGCGGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540  
 QY 541 CAGGACCCCGGATCTCGTAGTCCCGGCGCTCAATGAGCAACGCGGAGTGGCTCTCG 600  
 DB 541 CAGGACCCCGGATCTCGTAGTCCCGGCGCTCAATGAGCAACGCGGAGTGGCTCTCG 600  
 QY 660 CCGTGGCGCTGCGCGCGCTCTCTGAGCTCTGCGGGGCGCAACGCGCGTCCCGCGCTG 660

DB 601 CCTTCGCGCTGCTGCGCGCTCTGCTGCTGCGGGGCGCACCGCGCTCCCGCGCTCG 660  
 QY 661 GGGCCCGAGACCGCGGAGCGCGCGCGCTGTTCAAGCGCGCAATGCGGCGCGCGCG 720  
 DB 661 GGGCCCGAGACCGCGGAGCGCGCGCGCTGTTCAAGCGCGCAATGCGGCGCGCGCG 720  
 QY 721 CAGCTGGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780  
 DB 721 CAGCTGGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780  
 QY 781 CTGTGCTCAGCATCTCTTACGCGCTCAACGCGCGGAGCTGTGAGAGCACTGCGCG 840  
 DB 781 CTGTGCTCAGCATCTCTTACGCGCTCAACGCGCGGAGCTGTGAGAGCACTGCGCG 840  
 QY 841 CTGCGAGCGCGCGCGCTGCGCGCGCGGAGAGAGGCGCACCGGAGACCGCTCGCT 900  
 DB 841 CTGCGAGCGCGCGCGCTGCGCGCGCGGAGAGAGGCGCACCGGAGACCGCTCGCT 900  
 QY 901 CCGTAGTGAAGCGCGCGCTGCTCAAGAGCGCTGCTGCTGCGCGCGCGCGCGGAGC 960  
 DB 901 CCGTAGTGAAGCGCGCGCTGCTCAAGAGCGCTGCTGCTGCGCGCGCGCGCGGAGC 960  
 QY 961 GCGCAACGCGTGGTCCCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020  
 DB 961 GCGCAACGCGTGGTCCCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020  
 QY 1021 TTTCCTATTGCTGATTCAGCTCCACCGCGCG 1052  
 DB 1021 TTTCCTATTGCTGATTCAGCTCCACCGCGCG 1052

## RESULT 11

## AL137000

LOCUS AL137000 163284 bp DNA linear PRI 18-DEC-2000  
 DEFINITION Human DNA sequence from clone RP11-203116 on chromosome 13 contains the gene for KIA0970 protein, COX7C1 (cytochrome c oxidase subunit VIIc pseudogene 1), a novel pseudogene, the GPR38 (G protein-coupled receptor 38) gene, ESTs, STSs, GSSs and a Cpg island, complete sequence.

## ACCESSION

AL137000.6 GI:9944121

## VERSION

HTG: COX7C1; Cpg island; cytochrome c oxidase; G protein-coupled receptor; GPR38; KIA0970.

## KEYWORDS

receptor; GPR38; KIA0970.

## SOURCE

Homo sapiens (human)

## ORGANISM

Homo sapiens

## REFERENCE

Waller, M.

## AUTHORS

Submitted (18-DEC-2000) Sanger Centre, Hinxton, Cambridgeshire, UK

## TITLE

request: clonerequest@sanger.ac.uk

## JOURNAL

On Aug 29, 2000 this sequence version replaced gi:9926419.

## COMMENT

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

## REFERENCE

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

## REFERENCE

Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WormBase; Information on the WORMBASE database can be found at

## REFERENCE

http://www.sanger.ac.uk/Projects/C\_elegans/wormbase This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 Mapping Group. Further information can be found at

## REFERENCE

http://www.sanger.ac.uk/HGP/Chr13

## REFERENCE

IMPORTANT: This sequence is not the entire insert of clone RP11-203116 it may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.



## ALIGNMENTS

ID \_MTLR\_HUMAN STANDARD; PRT; 412 AA.

0C Mammalia; Butheria; Primates; Catarrhini; Homnidae; Homo.  
0C Chordata; Craniata; Vertebrata; Euteostomi;  
0S Homo sapiens (human).

|    |  |
|----|--|
| RP | SEQUENCE FROM N.A. (ISOFORMS A AND B).                                 |
| RK | MEIDLIN=99316084; PMID=10381885; DOI=10.1126/science.284.5423.2184;    |
| RA | Palghatkar S.D., Tan C.P., McKee K.K., Palyha O.C., Hreniuk D.L.,      |
| RA | Pong S.-S., Baskin C.P., Figueroa D., MacNeil D., Cascardi M.A.,       |
| RA | Naragund R., Baskin R., Abreu-Villa M., Socorro R., Kargman S.,        |
| RA | O'Neill G., van der Ploeg L.H.T., Evans J., Patchett A.A., Smith R.G., |
| RA | Howard A.D.,   |
| RT | Receptor for mottlin identified in the human gastrointestinal          |

RA Dunham A., Matthews L.H., Burton D., Amundsen C.T., Rose M.H.,  
RA Ashcroft K.D., Beare D.M., Burford D.C., Hunt S.B.,  
RA Griffiths-Jones S., Jones M.C., Keenan S.J., Oliver K., Scott C.B.,  
RA Almeida J.P., Amrose K.D., Andrews D.T.,  
RA Almswough R., Almeida J.P., Bagguley C.L., Bailey J., Bannmerjee R.,  
RA Ashwell R.I.S., Babbage A.K., Bagguley C.L., Bailey J., Bannmerjee R.,  
RA Batlow K.P., Bates K., Beasley H., Bird C.P., Bray-Allen S.,  
RA Brown A.U., Brown J.Y., Burrill W., Carder N.P., Carter N.P.,  
RA Chapman J.C., Clark M.B., Clark S.Y., Clarke G., Clee G.M.,  
RA Cobley V., Collins J.R., Corry N., Corry N., Coville J.C.,  
RA Cobley V., Collins J.R., Corry N., Corry N., Coville J.C.,

RA Mashreghi-Mohammadi M., McLaren S.J., McMurray A., Milne S.,  
RA Lloyd D.M., Lloyd C., Lovell J., Martin S.,  
RA King A., Latif G.K., Langford C.J., Lawlor S., Leongamert D.A.,  
RA Johnson C., Johnson D., Key M., Kimberley A.M.,  
RA Hunt P.J., Hunt A.R., Heath P.D., Howden P.J., Huckle B.J.,  
RA Harley J.T., Hart B.A.,  
RA Gratham D.V., Grigble S.M., Griffiths C., Hall R.B., Hammond S.,  
RA Garner P., Garnett J., Gilbert J.G.R., Gibson C.J., Giori J.,  
RA Rillingdon A.G., Faulkner L., Frankish A.G., Frankland J., French L.,  
RA Deloug S.C., Dhumi P., Dunham I., Dunn M., Eathrowl M.B.,  
RA Clegg S.C., Cohen J.,

```

RA Moore M.J.F., Nickerson T., Palmer S.A., Pearce A.V., Peck A.I.,  

RA Pelan S., Phillimore B., Porter K.M., Rice C.M., Seale S.,  

RA Sehra H.K., Showkeen R., Skuce C.D., Smith W., Steward C.A.,  

RA Symamoe N., Teesler J., Thomas D.W., Tracey A., Tromans E., Tubby B.,  

RA Wall M.E., Wallis J.M., West A.P., Whitehead S.T., Willey D.L.,  

RA Williams L., Weay P.W., Wright M.W., Young L., Coulson A., Durbin R.,  

RA Hubbard T., Sulston J.B., Beck S., Bentley D.R., Rogers J., Ross M.T.,  

RT "The DNA sequence and analysis of human chromosome 13,"  

RL Nature 428:522-528 (2004).  

RN [4]  

RP FUNCTION:  

RX MEDLINE=121219832; PubMed=11322507; DOI=10.1385/ENDO.14:1.009;  

RY Smith R.G., Leonard R., Bailey A.R.T., Palaya O.C., Reigner S.D.,  

SA Tan C.P., McKee K.K., Peng S.-S., Grifflin P.R., Howard A.D.,  

RT "Growth hormone secretagogue receptor family members and ligands,"  

RL Endocrine 14:9-14 (2001).  

CC -1- FUNCTION: Receptor for mectlin.  

CC CC  

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  

CC CC  

CC -1- ALTERNATIVE PRODUCTS:  

CC Event=Alternative splicing; Named isoforms=2;  

CC Name=A;  

CC IsoId=O43193-1; Sequence=Displayed;  

CC Name=B;  

CC IsoId=O43193-2; Sequence=VSP_001894;  

CC CC  

CC -1- TISSUE SPECIFICITY: Expressed only in thyroid, stomach, and bone  

CC marrow.  

CC CC  

CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  

CC -----  

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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  

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CC or send an email to license@ib-sib.ch).  

CC -----  

DR EMBL: AF034632; AAC26081.1; --  

DR EMBL: AL137000; CAC19107.1; --  

DR GeneW: HGNC:4495; MLNR.  

DR MIM: 602885; --  

DR GO: GO:0005887; C:integral to plasma membrane; TAS.  

DR GO: GO:0004949; F:g-protein coupled receptor activity; TAS.  

DR GO: GO:0007586; P:digestion; TAS.  

DR GO: GO:0007186; P:g-protein coupled receptor protein signaln. . ; TAS.  

DR InterPro: IPR000276; GPCR_Rhodopsn.  

DR Pfam: PF00001; Tcm 1; 1.  

DR PRINTS: PR00237; GPCRHODOPSIN.  

DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.  

DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.  

KW Alternative splicing; g-protein coupled receptor; Glycoprotein;  

KV Transmembrane.  

FT FT DOMAININ 1 35  

FT TRANSMEM 36 56  

FT DOMAIN 57 74  

FT TRANSMEM 75 94  

FT DOMAIN 95 112  

FT TRANSMEM 113 134  

FT DOMAIN 135 157  

FT TRANSMEM 158 178  

FT TRANSMEM 179 246  

FT DOMAIN 247 270  

FT TRANSMEM 271 298  

FT TRANSMEM 299 320  

FT DOMAIN 321 334  

FT TRANSMEM 335 358  

FT DOMAIN 359 412  

FT DISULFID 413 423  

FT CARBOHYD 424 435  

FT CARBOHYD 436 446  

FT CARBOHYD 447 457  

FT VASPLIC 458 468  


```

| FT                    | FT   | SEQUENCE   | 412 AA; | 45344 MW;          | Cl3PFe165012DEF3 CRC64; | TRRGSSGSIYNNLVLAIPRMONH1HKGFAFDVLLSTVL<br>(in isoform B).<br>/FTID=VSP_001894. |
|-----------------------|--|--|---------|--------------------|-------------------------|--|
| SO                    | SEQUENCE   |  |         |                    |                         |  |
| Query Match           |  |  | 77.4%;  | Score 1581;        | DB 1;                   | Length 412;  |
| Best Local Similarity |  |  | 100.0%; | Pred. No. 1,1e-99; |                         |  |
| Matches               | 300;   | Conservative   | 0;      | Mismatches         | 0;                      | Indels 0; Gaps 0   |
| QY                    | 1  | MGSPWNGSDGEGAREPPMPALPPCDBERRCSPPFLGALVPTAVCLCLFVGVSGANVTY | 60      |                    |                         |  |
| DB                    | 1  | MGSPWNGSDGEGAREPPMPALPPCDBERRCSPPFLGALVPTAVCLCLFVGVSGANVTY | 60      |                    |                         |  |
| QY                    | 61   | MLIRYRDMRTTNTLYLGSMVSDLLILGLPDLRYLRMRSPWVRGELLCSLYVGG      | 120     |                    |                         |  |
| DB                    | 61   | MLIRYRDMRTTNTLYLGSMVSDLLILGLPDLRYLRMRSPWVRGELLCSLYVGG      | 120     |                    |                         |  |
| QY                    | 121  | CTVATLLHMTLSTERYLATCRPIRARLYLRRRVRALIAVLAVALISAGFLFLVGV    | 180     |                    |                         |  |
| DB                    | 121  | CTVATLLHMTLSTERYLATCRPIRARLYLRRRVRALIAVLAVALISAGFLFLVGV    | 180     |                    |                         |  |
| QY                    | 181  | QDPGISVYPGLNGTARIASSPLASSPPLMLSRAPPPSPGSETAAALPSRECRPSPA   | 240     |                    |                         |  |
| DB                    | 181  | QDPGISVYPGLNGTARIASSPLASSPPLMLSRAPPPSPGSETAAALPSRECRPSPA   | 240     |                    |                         |  |
| QY                    | 241  | QLGALRYMLWTTNTYFFLPFLCLSLYLGLIRGLMLSSRRPLRGPAASGRGRHQTQRYL | 300     |                    |                         |  |
| DB                    | 241  | QLGALRYMLWTTNTYFFLPFLCLSLYLGLIRGLMLSSRRPLRGPAASGRGRHQTQRYL | 300     |                    |                         |  |
| RESULT 2              |  |  |         |                    |                         |  |
| Q6YGZ2                |  |  |         |                    |                         |  |
| Q6YGZ2                | PRELIMINARY;   | PRT;   | 295 AA. |                    |                         |  |
| ID                    | Q6YGZ2   |  |         |                    |                         |  |
| AC                    | 05-JUL-2004 (TREMBLrel. 27, Created)                                     |  |         |                    |                         |  |
| DT                    | 05-JUL-2004 (TREMBLrel. 27, Last sequence update)                        |  |         |                    |                         |  |
| DT                    | 05-JUL-2004 (TREMBLrel. 27, Last annotation update)                      |  |         |                    |                         |  |
| DT                    | 05-JUL-2004 (TREMBLrel. 27, Last annotation update)                      |  |         |                    |                         |  |
| DS                    | Growth hormone secretagogue receptor 1b.                                 |  |         |                    |                         |  |
| OS                    | Acanthopagrus schlegelii (Black porgy).                                  |  |         |                    |                         |  |
| OS                    | Acanthopagrus schlegelii (Black porgy).                                  |  |         |                    |                         |  |
| OC                    | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;        |  |         |                    |                         |  |
| OC                    | Actinopterygii; Neopteleostei; Teleostei; Euteleostei; Neocleostei;      |  |         |                    |                         |  |
| OC                    | Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Percoidae;    |  |         |                    |                         |  |
| OC                    | Sparidae; Acanthopagrus.   |  |         |                    |                         |  |
| OX                    | NCBI_TaxID=72011;  |  |         |                    |                         |  |
| RP                    | [1]  |  |         |                    |                         |  |
| RP                    | SEQUENCE FROM N.A.   |  |         |                    |                         |  |
| RX                    | PubMed=15062547; DOI=10.1016/j.mce.2003.11.020;                          |  |         |                    |                         |  |
| RA                    | Chan C.B.; Cheng C.H.K.;   |  |         |                    |                         |  |
| RT                    | "Identification and functional characterization of two alternatively     |  |         |                    |                         |  |
| RT                    | spliced growth hormone secretagogue receptor transcripts from the        |  |         |                    |                         |  |
| RT                    | placenta of black seabream Acanthopagrus schlegelii."                    |  |         |                    |                         |  |
| RL                    | Mol. Cell. Endocrinol. 214:81-95(2004).                                  |  |         |                    |                         |  |
| CC                    | -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).     |  |         |                    |                         |  |
| CC                    | -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.      |  |         |                    |                         |  |
| CC                    | EMBL; AY151041; AAN7876.1; -   |  |         |                    |                         |  |
| DR                    | GO; GO:0016021; C:Integral to membrane; IEA.                             |  |         |                    |                         |  |
| DR                    | GO; GO:0016520; F:growth hormone-releasing hormone receptor a. . .; IEA. |  |         |                    |                         |  |
| DR                    | GO; GO:0004872; F:receptor activity; IEA.                                |  |         |                    |                         |  |
| DR                    | GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.                 |  |         |                    |                         |  |
| DR                    | GO; GO:0007186; F:G-protein coupled receptor protein signaln. . .; IEA.  |  |         |                    |                         |  |
| DR                    | InterPro; IPR003905; GHS1_receptor.                                      |  |         |                    |                         |  |
| DR                    | InterPro; IPR000276; GPCR_Rhodpsn.                                       |  |         |                    |                         |  |
| DR                    | Pfam; PF00001; 7tm.1.1.  |  |         |                    |                         |  |
| DR                    | PRINTS; PRO1417; GHSRCDOPSN.   |  |         |                    |                         |  |
| DR                    | PRINTS; PRO0237; GPCRRODOPSN.  |  |         |                    |                         |  |
| DR                    | PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.                               |  |         |                    |                         |  |
| DR                    | PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1.                               |  |         |                    |                         |  |
| DR                    | KW   | G-protein coupled receptor; Receptor; Transmembrane.       |         |                    |                         |  |
| SO                    | SEQUENCE   | 295 AA; 33883 MW; E7397DCADDPF3873 CRC64;                  |         |                    |                         |  |
| Query Match           |  |  | 33.0%;  | Score 674;         | DB 2;                   | Length 295;  |
| Best Local Similarity |  |  | 45.3%;  | Pred. No. 3.9e-38; |                         |  |
| Matches               | 141;   | Conservative   | 43;     | Mismatches         | 73;                     | Indels 54; Gaps 7  |